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Poster Session V
Molecular diagnosis of respiratory tract bacterial infections

ROUTINE REAL-TIME PCR FOR LEGIONELLA SPECIES AND L. PNEUMOPHILA AS PART OF A FRONT-LINE SYNDROMIC MOLECULAR TESTING ALGORITHM FOR PNEUMONIA PATIENTS IN THE UK

N.J. Gadsby[1], K.O. Helgason[1], E.M. Dickson[2], J.M. Mills[3], D.S. Lindsay[4], G.F. Edwards[4], M.F. Hanson[1], **K.E. Templeton**[1]

[1]Medical Microbiology, Royal Infirmary of Edinburgh, Edinburgh, United Kingdom ; [2]Scottish MRSA Reference Laboratory, Glasgow Royal Infirmary, Glasgow, United Kingdom ; [3]Medical Microbiology, Raigmore Hospital, Inverness, United Kingdom ; [4]Scottish Haemophilus Legionella Meningococcus and Pneumococcus Reference Laboratory, Glasgow Royal Infirmary, Glasgow, United Kingdom

Objectives: *Legionella pneumophila* serogroup 1 (sg1) is the major cause of Legionnaires' Disease (LD) in Europe, although other serogroups and *Legionella* species are increasingly implicated. The most commonly used rapid diagnostic test for LD is the urinary antigen test, however, this is designed to detect only *L. pneumophila* sg1. Real-time PCR is now available for rapid detection of both *L. pneumophila* and *Legionella* species, but is not widely used in the routine diagnostic setting. The aim of the study was to determine the clinical and public health benefits of using *L. pneumophila* and *Legionella* species real-time PCR as part of a syndromic molecular testing algorithm in a front-line diagnostic laboratory.

Methods: Over a 44-month period between 2010 and 2013, 1944 specimens were tested by duplex *L. pneumophila* and *Legionella* species real-time PCR in the Microbiology laboratory of a large tertiary care hospital in Edinburgh, UK. The syndromic molecular testing algorithm for severe respiratory infection also included PCR for nine respiratory viruses along with the atypical bacterium *Mycoplasma pneumoniae*, standard microbiological culture methods and urinary antigen testing for *L. pneumophila* sg1.

Results: 49 (2.7%) specimens from 36 patients were *L. pneumophila* PCR positive; 28 were confirmed LD cases and 8 were probable cases. Optimal sensitivity (95.8%) and specificity (99.7%) for the detection of confirmed cases was achieved with *L. pneumophila* PCR and/or urinary antigen testing, compared with either test alone. The majority of *L. pneumophila* LD cases occurred during an outbreak of LD in Edinburgh in 2012. Using the syndromic respiratory molecular testing algorithm also led to the detection of 81 rhinovirus, 21 parainfluenza virus-3, 12 human metapneumovirus, 11 adenovirus and 16 other viral infections in patients with respiratory illness. A further 10 patients with severe pneumonia were PCR positive for *Legionella* species, 5 of whom were confirmed cases of *L. longbeachae* LD. Three of 5 probable *Legionella* species cases had a specific antibody response to *L. anisa, L. hackeliae* and *L. longbeachae* respectively.

Conclusion: *L. pneumophila* and *Legionella* species PCR has been a part of our syndromic respiratory molecular testing algorithm for patients with severe pneumonia for the last four years. This approach enabled early detection and rapid response to a large outbreak of LD and the identification of cases of severe pneumonia due to *Legionella* species, particularly *L. longbeachae*, which may otherwise have gone undetected with urinary antigen testing alone. Therefore, *L. pneumophila* and *Legionella* species PCR is a valuable addition to urinary antigen testing in the front-line diagnostic laboratory, as part of a well-defined algorithm. Furthermore, we propose that cases of LD due to *L. longbeachae* be considered laboratory-confirmed when there is a positive *Legionella* species PCR result and detection of *L. longbeachae* specific antibody response.